

Yu, K., Akimov, H., Shen, K., Gouvasakatos, S., Militischer, J., Adams, M.D., and Venter, J.C.
 A BAC End Sequence Database for Identifying Minimal Overlaps in Arabidopsis Genomic Sequencing. Update 4
 Arabidopsis Genomic Sequencing. Update 4
 Unpublished (1998)
 Contact: Steve Rounsley
 Department of Eukaryotic Genomics
 The Institute for Genomic Research
 9712 Medical Center Dr., Rockville, MD 20850, USA
 Tel: 401 838 0200
 Fax: 401 838 0200
 Email: rounsley@tigr.org
 Seq primer: M13 Reverse
 Class: BAC ends
 High quality sequence stop: 102.

FEATURES
 source
 1. 102
 /organism="Arabidopsis thaliana"
 /strain="Columbia"
 /db_xref="taxon:3702"
 /clone="F2367"
 /clone.lib="IGF"
 /sex="hermaphrodite"
 /note="Vector: HeLaAC11; Site_1: EcoRI; Site_2: EcoRI, produced by Thomas Aitmann"
 BASE COUNT 24 a 27 c 16 g 36 t
 ORIGIN

Alignment Scores:
 Pred. No.: 1,270-03 Length: 102
 Score: 24.00 Matches: 5
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DH: 17 Gaps: 0

US-09-856-070-18 (1-5) x AG010934 (1-102)

QY 1 LysGlutLeuMet 5
 A003501/c
 LOCUS
 DB 80 AAGACAGCTTATC 66

RESULT 2
 A1003501
 DEFINITION
 106 bp mRNA linear EST 09-JUN 1998
 IMAGE:1699097 3' similar to SW:CA1H_HUMAN P19060 COLLAGEN ALPHA 1(XVII) CHAIN ;, mRNA sequence.

ACCESSION
 A1003501
 VERSION
 A1003501.1 GI:3203040
 SOURCE
 EST.
 ORGANISM
 Homo sapiens

REFERENCE
 1 (bases 1 to 106)
 Miller, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Post, S., Kizman, D., Kucaba, T., Lacy, M., Lee, N., Lennox, G., Marra, M., Martin, J., Moore, H., Schellenger, K., Steptoe, M., Tan, F., Theising, B., White, Y., Wyllie, J., Waterston, R., and Wilson, R.
 WashU-NCI Human EST Project
 Unpublished (1997)
 Contact: Wilson R

TITLE
 JOURNAL
 COMMENT
 Washington University School of Medicine
 4444 Forest Park Parkway Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@wustl.edu
 This clone is available royalty free through LIRL. Contact the IMAGE Consortium (image.lirll.gov) for further information. Trace considered overall poor quality. Possible reversed clone; similarity on wrong strand

Seq primer: -40m13 fwd. FT from Amersham
 High quality sequence stop: 1.
 Location/Qualifiers
 1. 106

/organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:1699097"
 /clone.lib="Gessler Wilms tumor"
 /sex="pooled (6)"
 /lab_host="DH10B"

/note="Vector: pSP6911; Site_1: SalI; Site_2: NotI; RNA was prepared from a pool of 6 anonymous Wilms' tumor RNAs. RNA was prepared by acid-phenol, followed by one round of oligo dt selection. cDNA library preparation was with the BRL/Life Tech. Superscript Plasmid system. An oligo-dT NotI primer for first strand synthesis generated ggaacccc(t)n at the 3' end of the clones. A 5' SalI adaptor was used with sequence 5'-gtcaccacgacgac-3'. Resulting cDNAs were size selected (average size 2 kb), NotI digested, and ligated into NotI/SalI-cut pSP6911. Library was constructed by Dr. Manired Gessler."

BASE COUNT 22 a 26 c 28 g 30 t
 ORIGIN

Alignment Scores:
 Pred. No.: 1,340-03 Length: 106
 Score: 24.00 Matches: 5
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DH: 9 Gaps: 0

US-09-856-070-18 (1-5) x A1003501 (1-106)

QY 1 LysGlutLeuMet 5
 DB 64 AAGACAGCTTATC 50

RESULT 3
 A2825768
 LOCUS
 DEFINITION
 109 bp DNA linear GSS 20-FEB-2001
 clone UGC2M010108 F, DNA sequence.

ACCESSION
 A2825768
 VERSION
 A2825768.1 GI:12995676
 KEYWORDS
 GSS.
 SOURCE
 house mouse.
 ORGANISM
 Mus musculus

REFERENCE
 1 (bases 1 to 109)
 Fukuyoda, Y., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Dunn, D., Longacre, S., Mahmood, M., Meenu, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausen, A., and Wright, D., Weiss, R.
 Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
 Unpublished (2000)
 Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., Salt, UT 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddb@genetics.utah.edu
 Insert length: 10000 Std Error: 0.00
 Plate: 0101 Row: G Column: 08
 Seq primer: GGTGGTAAAGACAGCTTATC
 Class: plasmid ends
 High quality sequence stop: 109.

FEATURES
 source
 1. 109
 Location/Qualifiers

/organism="Mus musculus"
 /strain="057H1/6.1"
 /db_xref="taxon:10090"
 /clone="mug2w0101404"
 /clone_lib="Mouse 10kb plasmid UUCGIM library"
 /sex="Male"
 /lab_host "E. Coli strain XL10-Gold, TI-resistant, P-"
 /note="vector: pW042nv, Purified genomic DNA from M.
 musculus 057BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/) The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity the sheared DNA
 was blunt end-repaired with T4 DNA polymerase and 14
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of pW042 (g1147321141q1AF129072.1), a copy-number
 inducible derivative of plasmid p1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

BASE COUNT 29 a 15 c 34 g 31 t
 ORIGIN
 Alignment Scores:
 Prod. No.: 1.4e+03 Length: 109
 Score: 24.00 Matches: 5
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 17 Gaps: 0

US-09-856-070-18 (1-5) x A2425768 (1-109)

QY 1 LysGluGluLeuMet 5
 LOCUS
 |||||||

DB 79 AAGGAAGATTCATG 93

RESULT 4
 AW946335

LOCUS AW946335 115 bp mRNA linear EST 31-MAY-2000
 DEFINITION KC2-ET0018-206400-012-007 ET0018 Homo sapiens cDNA, mRNA sequence.
 ACCESSION AW946335
 VERSION AW946335.1 GI:8124101
 KEYWORDS EST.
 SOURCE human.

ORGANISM

Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catartini; Homidae; Homo.

REFERENCE

1 (bases 1 to 115)
 Dias Neto, E., Garcia Correa, R., Vetrjovsky-Almeida, S., Arlones, M.R.,
 Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,
 Goldman, G.H., Carvalho, A.F., Matsukuma, A., Balas, S., Simpson, D.H.,
 Brunstein, A., de Oliveira, P.S., Bucher, P., Tomazini, V., O'Hare
 M.J., Soares, F., Arentani, R.R., Reis, L.F., de Souza, S.J. and
 Simpson, A.J.
 Shotgun sequencing of the human transcriptome with ORF expressed
 sequence tags

TITLE

Shotgun sequencing of the human transcriptome with ORF expressed

JOURNAL

MEDLINE

COMMENT

Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

20202663

Contact: Simpson A.J.G.

Laboratory of Cancer Genetics

Ludwig Institute for Cancer Research

Rua Prof. Antonio Prudente 109, 4 andar, 01504-010, Sao Paulo-SP,

Brazil

Tel: +55-11-2704922

Fax: +55-11-2707001

Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/110CR Human Cancer Genome
 Project. This entry can be seen in the following URL
 (http://www.ludwig.org.br/scripts/gethtml.pl?1-512-002-ET0018 290
 400-011-cu/856-090-04-290414-1)

Seq primer: puc 18 forward

High quality sequence start: 9

High quality sequence stop: 115.

Location/Qualifiers

1..115

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone_lib="ET0018"

/dev_stage="Adult"

/note="Origin: lung_tumor. Vector: puc18. Site: 1: Small;

Site: 2: Small; A mini-library was made by cloning products

derived from ORESTES PCR (U.S. Letters Patent application

No. 196,716 - Ludwig Institute for Cancer Research)

profiles into the pUC 18 vector. Reverse transcription of

tissue mRNA and cDNA amplification were performed under

low stringency conditions."

BASE COUNT 38 a 20 c 24 g 33 t

ORIGIN

Alignment Scores:

Prod. No.: 1.51e+03 Length: 115

Score: 24.00 Matches: 5

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0

DB: 16 Gaps: 0

US-09-856-070-18 (1-5) x AW946335 (1-115)

QY 1 LysGluGluLeuMet 5

LOCUS

|||||||

DB 10 AAGGAAGAGCTCATG 24

RESULT 5

AZ761701/c

LOCUS

DEFINITION

127 bp DNA linear GSS 16-FEB-2001

IM0556707f Mouse 10kb plasmid UUCGIM library Mus musculus genomic

clone UUCGIM0556707 F, DNA sequence.

ACCESSION AZ761701

VERSION AZ761701.1 GI:12870903

KEYWORDS GSS.

SOURCE house mouse.

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

REFERENCE

AUTHORS

1 (bases 1 to 127)

Dunn, D., Anyagi, A., Barber, M., Beasorn, T., Duval, B., Hamil, C.,

Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly

M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.

and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished (2000)

CONTACT: Robert B. Weiss

University of Utah

Genome Center

RM. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: dunn@genetics.utah.edu

Insert length: 10000 Std Error: 0.00

Plate: 0556 row: J column: 07

Seq primer: GGTTCGTAAGAGCGCCAGT

Class: plasmid ends

High quality sequence stop: 127.

Location/Qualifiers

1..127

/organism="Mus musculus"

200000-110-411-581-4-0000-00-20014-1)

Seq primer: puc 18 forward

High quality sequence stop: 130.

Location/Qualifiers

Source

1. 130

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone_lib="ST0278"

/dev_stage="Adult"

Site 2: Smal: A mini library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the puc 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions.

44 a 25 c 35 g 26 t

BASE COUNT

ORIGIN

Alignment Scores:

Prod. No.: 1.8e+03 Length: 130
Score: 24.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 14 Gaps: 0

US-09-856-070-18 (1-5) x HQ364004 (1-130)

QY 1 LysGluGluLeuMet 5

Db 103 AAGAAGACGTGATG 117

RESULT 8

W86729/c

LOCUS

DEFINITION z63c11.1 Soares fetal_liver_spleen_LINLS.S1 Homo sapiens cDNA

clone IMAGE:416756.5' similar to SW1008_MOUSE P20456 BRAIN protein

DN38 ; mRNA sequence.

ACCESSION W86729

VERSION W86729.1 GI:1400477

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo;

1 (bases 1 to 136)

Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, R.,

Chissoe, S., Dietrich, N., DuBoque, T., Favell, A., Gish, W., Hawkins,

M., Hultman, M., Kucaba, T., Lacy, M., Le, M., Le, N., Mardis, E., Moore,

R., Morris, M., Parsons, J., Prange, C., Rifkin, J., Rohlfing, J.,

Schellenberg, K., Soares, M.B., Tan, F., Thierry-Mieg, J., Trevaskis, E.,

Underwood, K., Weidmann, P., Waterston, R., Wilson, R., and Maria, M.

Generation and analysis of 280,000 human expressed sequence tags

Genome Res 6 (9), 807-828 (1996)

97044478

CONTACT: Wilson RK

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 246 1800

Fax: 314 286 1810

Email: est@wustl.edu

This clone is available royalty-free through LINCS; contact the

IMAGE Consortium (infoimage.linc.gov) for further information.

Trace considered overall poor quality

Possible reversed clone similarity on wrong strand

Insert Length: 957 5' Error: 0.00

Seq primer: mab.PE3A+ET

High quality sequence stop: 1.

Location/Qualifiers

1. 136

/organism="Homo sapiens"

/db_xref="GDB:132526"

FEATURES

source

/db_xref="taxon:9606"
/clone_lib="Soares_fetal_liver_spleen_LINLS.S1"
/sex="male"
/dev_stage="20 week post conception fetus"
/lab_host="EBH103 (ampicillin resistant)"
/note="organ: Liver and Spleen; Vector: pT73D (Pharmacia)
with a modified polylinker; Site 1: Pac I; Site 2: Eco RI;
this is a subtracted version of the original Soares fetal
liver spleen LINLS library. 1st strand cDNA was primed
with a Pac I oligo(dT) primer 15'
AATGGAGAGATTAAATTAAGATCTTTTTTTTTTTTTTTT 3',
(Pharmacia), digested with Pac I and cloned into the Pac I
and Eco RI sites of the modified pT73 vector. Library
went through one round of normalization. Library
constructed by Renato Soares and M.Fatima Ronaldo."

BASE COUNT 32 a 25 c 22 g 54 t 3 others

ORIGIN

Alignment Scores:
Prod. No.: 1.92e+03 Length: 136
Score: 24.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 14 Gaps: 0

US-09-856-070-18 (1-5) x W86729 (1-136)

QY 1 LysGluGluLeuMet 5

Db 96 AAGAAGACGTTAATG 82

RESULT 9

BE774194/c

LOCUS

DEFINITION X91-00000-180000-014-b10 UM0009 Homo sapiens cDNA, mRNA sequence.

ACCESSION BE774194

VERSION BE774194.1 GI:10227758

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo;

1 (bases 1 to 137)

Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,

Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.,

Goldman, G.B., Carvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H.,

Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare

M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and

Simpson, A.J.

Shotgun sequencing of the human transcriptome with 3Kt expressed

sequence tags

Proc Natl Acad Sci U S A 97 (7): 3491-3496 (2000)

20202663

CONTACT: Simpson A.J.G.

Ludwig Institute for Cancer Research

Poa Prof. Antonio Prudente 109, 4 andar, 01500-010, Sao Paulo SP,

Brazil

Tel: +55-11-2704922

Fax: +55-11-2707001

Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/ILIC Human Cancer Genome

Project. This entry can be seen in the following URL

(http://www.ludwig.org.br/scripts/gethtml?plot=at2-MPL-000094-180

500-014-11051-2000-05-18&t4-1)

Seq primer: puc 18 forward

High quality sequence stop: 40

High quality sequence stop: 137.

Location/Qualifiers

1. 137

```

/organism "Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="HM0009"
/dev_stage="Adult"
/notes="ordan: uterus; Vector: puc18; Site:1; SmaI; Site:2;
SmaI: A mini-library was made by cloning products derived
from GRESIES PCR (U.S. Letters Patent application No. 196
716 - Ludwig Institute for Cancer Research) profiles
into the pUC 18 vector. Reverse transcription of tissue
mRNA and cDNA amplification were performed under low
stringency conditions."
BASE COUNT      26 a      42 c      29 g      50 t
ORIGIN
|||||
Alignment Scores:
Pred. No.:      1.94e-04      Length:      137
Score:          24.00      Matches:      5
Percent Similarity: 100.00%      Conservative: 0
Best local Similarity: 100.00%      Mismatches: 0
Query Match:      100.00%      Indels:      0
DB:              12      Gaps:      0

US-09-856-070-18 (1-5) x BE774194 (1-137)

QY      1  lvsGluGluGluMet 5
|||||
DB      73  AAGGAGGAGTGCATG 59

RESULT 10
LOCUS   BH811366
DEFINITION   SALK_058499 Arabidopsis thaliana DNA insertion lines Arabidopsis
thaliana genomic clone SALK_058499, DNA sequence.
ACCESSION   BH811366
VERSION     BH811366.1  GI:20489821
KEYWORDS    GSS
SOURCE      thale cress.
ORGANISM    Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta, eucolecyledons, core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 138)
REFERENCE   1  (bases 1 to 138)
AUTHORS    Alonso,J.M., Leisse,J.J., Barajas,P., Chen,H., Cheuk,K., Gadrinac,
J.C., Jesko,A., Karnes,M., Kim,C.J., Parker,H., Prentiss,L., Shinn,P.,
Zimmerman,J. and Ecker,J.R.
A Sequence-Indexed Library of Insertion Mutations in the
Arabidopsis Genome
Unpublished (2001)
Contact: Joseph A. Ecker
Salk Institute Genomic Analysis Laboratory (SIGAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6479
Email: ecker@salk.edu
This is single pass sequence recovered from the left border of
TUNA. This sequence lies within an annotated exon of At3g17740
Class: TUNA tagged.
Location/Qualifiers
1..138
/organism="Arabidopsis thaliana"
/strain="Columbia 0"
/db_xref="taxon:3702"
/clone_lib="SALK_058499"
/notes="new was performed on Arabidopsis thaliana lines
each of which contains one or more DNA insertion
elements. the resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. details of the protocols used can
be found at http://salk.edu/04na_projects.html"
BASE COUNT      40 a      47 c      25 g      36 t
ORIGIN
|||||
/organism "Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="ET0019"
/dev_stage="Adult"
/notes="ordan: lung tumor. Vector: puc18; Site:1; SmaI;
Site:2; SmaI: A mini-library was made by cloning products
derived from GRESIES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
BASE COUNT      48 a      24 c      31 g      36 t
ORIGIN
|||||
Alignment Scores:
Pred. No.:      1.98e-03      Length:      140
Score:          24.00      Matches:      5
Percent Similarity: 100.00%      Conservative: 0
Best local Similarity: 100.00%      Mismatches: 0
Query Match:      100.00%      Indels:      0
DB:              17      Gaps:      0

US-09-856-070-18 (1-5) x BH811366 (1-138)

QY      1  lvsGluGluGluMet 5
|||||
DB      67  AAGGAGGAGTGCATG 53

RESULT 11
LOCUS   AW946443
DEFINITION   952-ET0019-090509-012 f12 ET0019 Homo sapiens cDNA, mRNA sequence.
ACCESSION   AW946443
VERSION     AW946443.1  GI:8124212
KEYWORDS    EST.
SOURCE      human.
ORGANISM    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 139)
REFERENCE   1  (bases 1 to 139)
AUTHORS    Dias Neto,E., Garcia Correa,R., Verjovsky-Almeida,S., Briones,M.R.,
Naai,M.A., da Silva,W. Jr., Zado,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Hucher,P., Jonqueiro,C.V., O'Hare
,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J.
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?c1=342-ec2-ET0019-080
509-012-f12&t3=2000-05-08&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 13
High quality sequence stop: 139.
Location/Qualifiers
1..139
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="ET0019"
/dev_stage="Adult"
/notes="ordan: lung tumor. Vector: puc18; Site:1; SmaI;
Site:2; SmaI: A mini-library was made by cloning products
derived from GRESIES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
BASE COUNT      48 a      24 c      31 g      36 t
ORIGIN
|||||
Alignment Scores:
Pred. No.:      1.98e-03      Length:      140
Score:          24.00      Matches:      5
Percent Similarity: 100.00%      Conservative: 0
Best local Similarity: 100.00%      Mismatches: 0
Query Match:      100.00%      Indels:      0
DB:              17      Gaps:      0

```


Search completed: January 16, 2003, 21:37:05
Job time : 664.571 secs

